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Display GenBank  Show 5  Send to  Hide:  sequence  all but gene, CDS and mRNA  
 Range: from  to   Reverse complemented strand Features:  SNP  MGC

1: BC016974. Reports Homo sapiens beta...[gi:16877455]

Links

Comment Features Sequence

LOCUS BC016974 1887 bp mRNA linear PRI 09-NOV-2001  
 DEFINITION Homo sapiens, clone IMAGE:4393885, mRNA, partial cds.  
 ACCESSION BC016974  
 VERSION BC016974.1 GI:16877455  
 KEYWORDS .  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 1887)  
 AUTHORS Strausberg, R.  
 TITLE Direct Submission  
 JOURNAL Submitted (05-NOV-2001) National Institutes of Health, Mammalian  
 Gene Collection (MGC), Cancer Genomics Office, National Cancer  
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
 USA  
 REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 COMMENT Contact: MGC help desk  
 Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: DCTD/DTP  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome  
 Center, Stanford University School of Medicine, Stanford, CA 94305  
 Web site: <http://www-shgc.stanford.edu>  
 Contact: (Dickson, Mark) mcd@paxil.stanford.edu  
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,  
 R. M.

Clone distribution: MGC clone distribution information can be found  
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Series: IRAK Plate: 27 Row: b Column: 11  
 This clone was selected for full length sequencing because it  
 passed the following selection criteria: GenomeScan gene  
 prediction.

Differences found between this sequence and the human reference  
 genome (build 36) are described in misc\_difference features below.

FEATURES	Location/Qualifiers
source	1..1887 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606"

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/tissue_type="Breast, mammary adenocarcinoma."
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/note="Vector: pCMV-SPORT6"
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/codon_start=3
/product="Unknown (protein for IMAGE:4393885)"
/protein_id="AAH16974.1"
/db_xref="GI:16877456"
/translation="RSGAGSCEEPSRRRRARGRACSEWSLVSRRPSVSALAGPLPLRR
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HELRNVIIRSTWMRHLQHPTLSQRVLVKFIIGAHGCEVPVEDREDPYSCKLLNITNPV
LNQEIEAFSLSEDTSGLPEDRVVSFSRVLYPIVITSLGVFYDANDVGFQRNITVKL
YQAEQEEALFIARFSPPSCGVQNKLWYKPVEQFILPESFEGTIVWESQDLHGLVSRN
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1875..1887
/note="polyA tail: 13 bases do not align to the human
genome."
```

## ORIGIN

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181 ggctgggtgt gctgtgccc tggtgtctcg gggccgcgt gcacctctgg ctgcggctgc  
241 gctcccccggc gcccgcctgc gcctccgggg ccggccctgc aggtggagtc tcactcttg  
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361 caagagattc tcctgcctca gcctcccaag tagctggat aacagatcag ttggccttat  
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661 atcaggaaat tgaagcgttc agtctgtccg aagacacttc atcggggctg cctgaggatc  
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841 aacaagagga ggcctcttc attgctcgct tcagtcctcc aagctgttgt gtgcaggtga  
901 acaagctgtg gtacaagccc gtggaaacaat tcatcttacc agagagctt gaaggtacaa  
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1801 agtataatgag gattcttagtt tctccatattt cttgtcaaca cttaaaaat tttgtttaaat  
1861 taaaatataa ccaaaaaaaaaaaaaaaa

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Range: from  to  Features:  CDD

1: Q8NCR0. Reports UDP-GalNAc:beta-1...[gi:74751196]

BLink, Conserved Domains, Links

Comment	Features	Sequence
LOCUS	Q8NCR0	500 aa linear PRI 04-DEC-2007
DEFINITION	UDP-GalNAc:beta-1,3-N-acetylgalactosaminyltransferase 2 (Beta-1,3-N-acetylgalactosaminyltransferase II) (Beta-3-GalNAc-T2).	
ACCESSION	Q8NCR0	
VERSION	Q8NCR0.1 GI:74751196	
DBSOURCE	swissprot: locus B3GL2_HUMAN, accession <a href="#">Q8NCR0</a> ; class: standard. extra accessions:Q59GR3,Q5TCI3,Q96AL7 created: Sep 5, 2006. sequence updated: Oct 1, 2002. annotation updated: Dec 4, 2007. xrefs: <a href="#">AL135928.6</a> , <a href="#">CAI21727.1</a> , <a href="#">CAI21728.1</a> , <a href="#">BC016974.1</a> , <a href="#">AAH16974.1</a> , <a href="#">BC029564.1</a> , <a href="#">AAH29564.1</a> , <a href="#">AB209046.1</a> , <a href="#">BAD92283.1</a> xrefs (non-sequence databases): RefSeq: <a href="#">NP_689703.1</a> , UniGene: <a href="#">Hs.585040</a> , Ensembl: <a href="#">ENSG00000162885</a> , GeneID: <a href="#">148789</a> , KEGG: <a href="#">hsa:148789</a> , HGNC: <a href="#">28596</a> , MIM: <a href="#">610194</a> , PharmGKB: <a href="#">PA142672567</a> , ArrayExpress: <a href="#">Q8NCR0</a> , CleanEx: <a href="#">HS_B3GALNT2</a> , GermOnline: <a href="#">ENSG00000162885</a> , InterPro: <a href="#">IPR002659</a> , PANTHER: <a href="#">PTHR11214</a> , Pfam: <a href="#">PF01762</a>	
KEYWORDS	Alternative splicing; Glycoprotein; Glycosyltransferase; Golgi apparatus; Membrane; Polymorphism; Signal-anchor; Transferase; Transmembrane.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.
REFERENCE	1 (residues 1 to 500)	
AUTHORS	Gregory, S.G., Barlow, K.F., McLay, K.E., Kaul, R., Swarbreck, D., Dunham, A., Scott, C.E., Howe, K.L., Woodfine, K., Spencer, C.C., Jones, M.C., Gillson, C., Searle, S., Zhou, Y., Kokocinski, F., McDonald, L., Evans, R., Phillips, K., Atkinson, A., Cooper, R., Jones, C., Hall, R.E., Andrews, T.D., Lloyd, C., Ainscough, R., Almeida, J.P., Ambrose, K.D., Anderson, F., Andrew, R.W., Ashwell, R.I., Aubin, K., Babbage, A.K., Bagguley, C.L., Bailey, J., Beasley, H., Bethel, G., Bird, C.P., Bray-Allen, S., Brown, J.Y., Brown, A.J., Buckley, D., Burton, J., Bye, J., Carder, C., Chapman, J.C., Clark, S.Y., Clarke, G., Clee, C., Cobley, V., Collier, R.E., Corby, N., Coville, G.J., Davies, J., Deadman, R., Dunn, M., Earthrow, M., Ellington, A.G., Errington, H., Frankish, A., Frankland, J., French, L., Garner, P., Garnett, J., Gay, L., Ghori, M.R., Gibson, R., Gilby, L.M., Gillett, W., Glithero, R.J., Grafham, D.V., Griffiths, C.,	

Griffiths-Jones, S., Grocock, R., Hammond, S., Harrison, E.S., Hart, E., Haugen, E., Heath, P.D., Holmes, S., Holt, K., Howden, P.J., Hunt, A.R., Hunt, S.E., Hunter, G., Isherwood, J., James, R., Johnson, C., Johnson, D., Joy, A., Kay, M., Kershaw, J.K., Kibukawa, M., Kimberley, A.M., King, A., Knights, A.J., Lad, H., Laird, G., Lawlor, S., Leongamornlert, D.A., Lloyd, D.M., Loveland, J., Lovell, J., Lush, M.J., Lyne, R., Martin, S., Mashreghi-Mohammadi, M., Matthews, L., Matthews, N.S., McLaren, S., Milne, S., Mistry, S., Moore, M.J., Nickerson, T., O'Dell, C.N., Oliver, K., Palmeiri, A., Palmer, S.A., Parker, A., Patel, D., Pearce, A.V., Peck, A.I., Pelan, S., Phelps, K., Phillimore, B.J., Plumb, R., Rajan, J., Raymond, C., Rouse, G., Saenphimmachak, C., Sehra, H.K., Sheridan, E., Shownkeen, R., Sims, S., Skuce, C.D., Smith, M., Steward, C., Subramanian, S., Sycamore, N., Tracey, A., Tromans, A., Van Helmond, Z., Wall, M., Wallis, J.M., White, S., Whitehead, S.L., Wilkinson, J.E., Willey, D.L., Williams, H., Wilmng, L., Wray, P.W., Wu, Z., Coulson, A., Vaudin, M., Sulston, J.E., Durbin, R., Hubbard, T., Wooster, R., Dunham, I., Carter, N.P., McVean, G., Ross, M.T., Harrow, J., Olson, M.V., Beck, S., Rogers, J., Bentley, D.R., Banerjee, R., Bryant, S.P., Burford, D.C., Burrill, W.D., Clegg, S.M., Dhami, P., Dovey, O., Faulkner, L.M., Gribble, S.M., Langford, C.F., Pandian, R.D., Porter, K.M. and Prigmore, E.

TITLE	The DNA sequence and biological annotation of human chromosome 1
JOURNAL	Nature 441 (7091), 315-321 (2006)
PUBMED	<u>16710414</u>
REMARK	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]. Erratum: [Nature. 2006 Oct 26;443(7114):1013. Banerjee, R [added]; Bryant, SP [added]; Burford, DC [added]; Burrill, WDH [added]; Clegg, SM [added]; Dhami, P [added]; Dovey, O [added]; Faulkner, LM [added]; Gribble, SM [added]; Langford, CF [added]; Pandian, RD [added]; Porter, KM [added]; Prigmore, E [added]] 2 (residues 1 to 500)
REFERENCE	
AUTHORS	Gerhard, D.S., Wagner, L., Feingold, E.A., Shenmen, C.M., Grouse, L.H., Schuler, G., Klein, S.L., Old, S., Rasooly, R., Good, P., Guyer, M., Peck, A.M., Derge, J.G., Lipman, D., Collins, F.S., Jang, W., Sherry, S., Feolo, M., Misquitta, L., Lee, E., Rotmistrovsky, K., Greenhut, S.F., Schaefer, C.F., Buetow, K., Bonner, T.I., Haussler, D., Kent, J., Kiekhaus, M., Furey, T., Brent, M., Prange, C., Schreiber, K., Shapiro, N., Bhat, N.K., Hopkins, R.F., Hsie, F., Driscoll, T., Soares, M.B., Casavant, T.L., Scheetz, T.E., Brown-stein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Piao, Y., Dudekula, D.B., Ko, M.S., Kawakami, K., Suzuki, Y., Sugano, S., Gruber, C.E., Smith, M.R., Simmons, B., Moore, T., Waterman, R., Johnson, S.L., Ruan, Y., Wei, C.L., Mathavan, S., Gunaratne, P.H., Wu, J., Garcia, A.M., Hulyk, S.W., Fuh, E., Yuan, Y., Snead, A., Kowis, C., Hodgson, A., Muzny, D.M., McPherson, J., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madari, A., Young, A.C., Wetherby, K.D., Granite, S.J., Kwong, P.N., Brinkley, C.P., Pearson, R.L., Bouffard, G.G., Blakesly, R.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Griffith, M., Griffith, O.L., Krzywinski, M.I., Liao, N., Morin, R., Palmquist, D., Petrescu, A.S., Skalska, U., Smailus, D.E., Stott, J.M., Schnurch, A., Schein, J.E., Jones, S.J., Holt, R.A., Baross, A., Marra, M.A., Clifton, S., Makowski, K.A., Bosak, S. and Malek, J.
CONSRTM	MGC Project Team
TITLE	The status, quality, and expansion of the NIH full-length cDNA project: the Mammalian Gene Collection (MGC)
JOURNAL	Genome Res. 14 (10B), 2121-2127 (2004)
PUBMED	<u>15489334</u>
REMARK	NUCLEOTIDE SEQUENCE [LARGE SCALE mRNA] (ISOFORMS 1 AND 2).

TISSUE=Mammary gland, and Testis  
 Erratum:[Genome Res. 2006 Jun;16(6):804. Morrin, Ryan [corrected to  
 Morin, Ryan]]  
 REFERENCE 3 (residues 1 to 500)  
 AUTHORS Totoki,Y., Toyoda,A., Takeda,T., Sakaki,Y., Tanaka,A., Yokoyama,S.,  
 Ohara,O., Nagase,T. and Kikuno,R.F.  
 TITLE Direct Submission  
 JOURNAL Submitted (??-MAR-2005)  
 REMARK NUCLEOTIDE SEQUENCE [LARGE SCALE mRNA] OF 74-500 (ISOFORM 1).  
 TISSUE=Brain  
 REFERENCE 4 (residues 1 to 500)  
 AUTHORS Hiruma,T., Togayachi,A., Okamura,K., Sato,T., Kikuchi,N.,  
 Kwon,Y.D., Nakamura,A., Fujimura,K., Gotoh,M., Tachibana,K.,  
 Ishizuka,Y., Noce,T., Nakanishi,H. and Narimatsu,H.  
 TITLE A novel human beta1,3-N-acetylgalactosaminyltransferase that  
 synthesizes a unique carbohydrate structure, GalNAcbeta1-3GlcNAc  
 J. Biol. Chem. 279 (14), 14087-14095 (2004)  
 PUBMED [14724282](#)  
 REMARK FUNCTION, BIOPHYSICOCHEMICAL PROPERTIES, GLYCOSYLATION, AND TISSUE  
 SPECIFICITY.  
 REFERENCE 5 (residues 1 to 500)  
 AUTHORS Sjoblom,T., Jones,S., Wood,L.D., Parsons,D.W., Lin,J., Barber,T.D.,  
 Mandelker,D., Leary,R.J., Ptak,J., Silliman,N., Szabo,S.,  
 Buckhaults,P., Farrell,C., Meeh,P., Markowitz,S.D., Willis,J.,  
 Dawson,D., Willson,J.K., Gazdar,A.F., Hartigan,J., Wu,L., Liu,C.,  
 Parmigiani,G., Park,B.H., Bachman,K.E., Papadopoulos,N.,  
 Vogelstein,B., Kinzler,K.W. and Velculescu,V.E.  
 TITLE The consensus coding sequences of human breast and colorectal  
 cancers  
 JOURNAL Science 314 (5797), 268-274 (2006)  
 PUBMED [16959974](#)  
 REMARK VARIANT [LARGE SCALE ANALYSIS] SER-203.  
 COMMENT On or before Sep 7, 2006 this sequence version replaced  
gi:74707488, gi:74746072, gi:74731130.  
 [FUNCTION] Beta-1,3-N-acetylgalactosaminyltransferase active in  
 synthesizing a unique carbohydrate structure,  
 GalNAc-beta-1-3GlcNAc, on N- and O-glycans. Has no galactose nor  
 galactosaminyl transferase activity toward any acceptor substrate.  
 [BIOPHYSICOCHEMICAL PROPERTIES] Kinetic parameters: KM=5.4 uM for  
 UDP-GalNAc; KM=11 mM for GlcNAc-beta-Bn.  
 [PATHWAY] Protein modification; protein glycosylation.  
 [SUBCELLULAR LOCATION] Golgi apparatus membrane; Single-pass type  
 II membrane protein (By similarity).  
 [ALTERNATIVE PRODUCTS] Event=Alternative splicing; Named  
 isoforms=2; Name=1; IsoId=Q8NCR0-1; Sequence=Displayed; Name=2;  
 IsoId=Q8NCR0-2; Sequence=VSP\_020250, VSP\_020251, VSP\_020252;  
 Note=No experimental confirmation available.  
 [TISSUE SPECIFICITY] Expressed in all tissues examined, but at  
 highest levels in testis, adipose tissue, skeletal muscle and  
 ovary.  
 [PTM] N-glycosylated (Probable).  
 [SIMILARITY] Belongs to the glycosyltransferase 31 family.  
 [WEB RESOURCE] Name=GGDB; Note=GlycoGene database;  
 URL='<http://ggdb.muse.aist.go.jp/GGDB/index.jsp>'.

FEATURES	Location/Qualifiers
source	1..500 /organism="Homo sapiens" /db_xref="taxon:9606"
gene	1..500 /gene="B3GALNT2"

Protein 1..500  
/gene="B3GALNT2"  
/product="UDP-GalNAc:beta-1,  
3-N-acetylgalactosaminyltransferase 2"  
/EC\_number="2.4.1.-"

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/region\_name="Mature chain"  
/experiment="experimental evidence, no additional details recorded"  
/note="UDP-GalNAc:beta-1,3-N-acetylgalactosaminyltransferase 2. /FTId=PRO\_0000248362."

Region 1..6  
/gene="B3GALNT2"  
/region\_name="Topological domain"  
/inference="non-experimental evidence, no additional details recorded"  
/note="Cytoplasmic (Potential)."

Region 7..23  
/gene="B3GALNT2"  
/region\_name="Transmembrane region"  
/inference="non-experimental evidence, no additional details recorded"  
/note="Signal-anchor for type II membrane protein (Potential)."

Region 24..500  
/gene="B3GALNT2"  
/region\_name="Topological domain"  
/inference="non-experimental evidence, no additional details recorded"  
/note="Lumenal (Potential)."

Region 37  
/gene="B3GALNT2"  
/region\_name="Splicing variant"  
/experiment="experimental evidence, no additional details recorded"  
/note="A -> AGGVSLLLPRLECNGAVSAHPNLHLPGSRDSPASAS QVAGIT (in isoform 2). /FTId=VSP\_020250."

Site 116  
/gene="B3GALNT2"  
/site\_type="glycosylation"  
/inference="non-experimental evidence, no additional details recorded"  
/note="N-linked (GlcNAc...) (Potential)."

Site 174  
/gene="B3GALNT2"  
/site\_type="glycosylation"  
/inference="non-experimental evidence, no additional details recorded"  
/note="N-linked (GlcNAc...) (Potential)."

Region 203  
/gene="B3GALNT2"  
/region\_name="Variant"  
/experiment="experimental evidence, no additional details recorded"  
/note="N -> S (in a breast cancer sample; somatic mutation). /FTId=VAR\_035860."

Region 281..285  
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/region\_name="Splicing variant"

/experiment="experimental evidence, no additional details recorded"  
/note="EGDAL -> GKFAS (in isoform 2). /FTId=VSP\_020251."  
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/gene="B3GALNT2"  
/region\_name="Splicing variant"  
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/note="Missing (in isoform 2). /FTId=VSP\_020252."  
Region  
307..457  
/gene="B3GALNT2"  
/region\_name="Galactosyl\_T"  
/note="Galactosyltransferase. This family includes the galactosyltransferases UDP-galactose:2-acetamido-2-deoxy-D-glucose3beta-galactosyltransferase and UDP-Gal:beta-GlcNAc beta 1,3-galactosyltranferase; pfam01762"  
/db\_xref="CDD:85659"

## ORIGIN

1 mrnwlvllcp cvlgaahlw lrlrspppac asgagpadql alfpqwksth ydvvvgvlsa  
61 rnnhelrnvi rstwmrhlq hptlsqrvlv kfiigahgce vpvedredpy sckllnitnp  
121 vlnqeieafs lsedtssglp edrvvsvsfr vlypivitsl gvfydandvg fqrnitvkly  
181 qaeqeealfi arfspsscgv qvnklwykpv eqfilpesfe gtivwesql hglvsrnlhk  
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301 rnlheedall keessiyddi vfvvdvvdtyr nvpakllnfv rwtvettsfn lllktdddry  
361 idleavfnri vqknldgpnf wwgfnrlnwa vdrtgkwqel eypspaypaf acgsgyvisk  
421 divkwlasns grlktyqged vsmgiwmaai gpkryqdslw lcektcetgm lsspqyspwe  
481 ltelwlker cgdpcrcqar

//

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Display GenBank  Show 5  Send to  Hide:  sequence  all but gene, CDS and mRNA

Range: from  to   Reverse complemented strand Features:

1: AK035259. Reports *Mus musculus* adul...[gi:26330547]

Links

Comment Features Sequence

LOCUS AK035259 2399 bp mRNA linear HTC 05-DEC-2002  
 DEFINITION *Mus musculus* adult male urinary bladder cDNA, RIKEN full-length enriched library, clone:9530006I10 product:hypothetical Glycosyltransferase family 31 containing protein, full insert sequence.  
 ACCESSION AK035259  
 VERSION AK035259.1 GI:26330547  
 KEYWORDS HTC; CAP trapper.  
 SOURCE *Mus musculus* (house mouse)  
 ORGANISM *Mus musculus*  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1  
 AUTHORS Carninci,P. and Hayashizaki,Y.  
 TITLE High-efficiency full-length cDNA cloning  
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
 PUBMED 10349636  
 REFERENCE 2  
 AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
 PUBMED 11042159  
 REFERENCE 3  
 AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.  
 TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer  
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)  
 PUBMED 11076861  
 REFERENCE 4  
 AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H.,

Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.

TITLE Functional annotation of a full-length mouse cDNA collection  
JOURNAL Nature 409 (6821), 685-690 (2001)  
PUBMED [11217851](#)  
REFERENCE 5  
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.  
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
JOURNAL Nature 420, 563-573 (2002)  
REFERENCE 6 (bases 1 to 2399)  
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.  
TITLE Direct Submission  
JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:<http://genome.gsc.riken.go.jp/>, Tel:81-45-503-9222, Fax:81-45-503-9216)  
COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
Please visit our web site for further details.  
URL:<http://genome.gsc.riken.go.jp/>  
URL:<http://fantom.gsc.riken.go.jp/>.  
FEATURES Location/Qualifiers  
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2341 ttttatgca acttgtgata ataaatattc tctatTTTAA aataaactag cttttccg

//

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Aug 28 2007 16:53:42

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Range: from  to  Features:  CDD

1: Q8BG28. Reports UDP-GalNAc:beta-1...[gi:81895977]

BLink, Conserved Domains, Links

Comment	Features	Sequence
LOCUS	Q8BG28	504 aa linear ROD 23-OCT-2007
DEFINITION	UDP-GalNAc:beta-1,3-N-acetylgalactosaminyltransferase 2 (Beta-1,3-N-acetylgalactosaminyltransferase II) (Beta-3-GalNAc-T2) (mbeta-3-GalNAc-T2).	
ACCESSION	Q8BG28	
VERSION	Q8BG28.1 GI:81895977	
DBSOURCE	swissprot: locus B3GL2_MOUSE, accession <u><a href="#">Q8BG28</a></u> ; class: standard. extra accessions:Q5U4F9,Q8BXL0 created: Sep 5, 2006. sequence updated: Mar 1, 2003. annotation updated: Oct 23, 2007. <u>xrefs: AB116655.1, BAD13421.1, AK035259.1, BAC29004.1, AK041022.1,</u> <u>BAC30784.1, AK044785.1, BAC32091.1, AK084275.1, BAC39153.1,</u> <u>AK151677.1, BAE30602.1, AK153362.1, BAE31934.1, AK167635.1,</u> <u>BAE39686.1, BC085110.1, AAH85110.1</u> <u>xrefs (non-sequence databases): RefSeq:NP_848755.1,</u> <u>UniGene:Mm.21686, Ensembl:ENSMUSG00000039242, GeneID:97884,</u> <u>KEGG:mmu:97884, MGI:2145517, ArrayExpress:Q8BG28,</u> <u>GermOnline:ENSMUSG00000039242, InterPro:IPR002659,</u> <u>PANTHER:PTHR11214, Pfam:PF01762</u>	
KEYWORDS	Alternative splicing; Glycoprotein; Glycosyltransferase; Golgi apparatus; Membrane; Signal-anchor; Transferase; Transmembrane.	
SOURCE	Mus musculus (house mouse)	
ORGANISM	<u>Mus musculus</u> Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.	
REFERENCE	1 (residues 1 to 504)	
AUTHORS	Hiruma,T., Togayachi,A., Okamura,K., Sato,T., Kikuchi,N., Kwon,Y.D., Nakamura,A., Fujimura,K., Gotoh,M., Tachibana,K., Ishizuka,Y., Noce,T., Nakanishi,H. and Narimatsu,H.	
TITLE	A novel human beta1,3-N-acetylgalactosaminyltransferase that synthesizes a unique carbohydrate structure, GalNAcbeta1-3GlcNAc	
JOURNAL	J. Biol. Chem. 279 (14), 14087-14095 (2004)	
PUBMED	<u>14724282</u>	
REMARK	NUCLEOTIDE SEQUENCE [mRNA] (ISOFORM 1), AND TISSUE SPECIFICITY.	
REFERENCE	2 (residues 1 to 504)	
AUTHORS	Carninci,P., Kasukawa,T., Katayama,S., Gough,J.; Frith,M.C., Maeda,N., Oyama,R., Ravasi,T., Lenhard,B., Wells,C., Kodzius,R., Shimokawa,K., Bajic,V.B., Brenner,S.E., Batalov,S., Forrest,A.R., Zavolan,M., Davis,M.J., Wilming,L.G., Aidinis,V., Allen,J.E.,	

Ambesi-Impiombato,A., Apweiler,R., Aturaliya,R.N., Bailey,T.L., Bansal,M., Baxter,L., Beisel,K.W., Bersano,T., Bono,H., Chalk,A.M., Chiu,K.P., Choudhary,V., Christoffels,A., Clutterbuck,D.R., Crowe,M.L., Dalla,E., Dalrymple,B.P., de Bono,B., Della Gatta,G., di Bernardo,D., Down,T., Engstrom,P., Fagiolini,M., Faulkner,G., Fletcher,C.F., Fukushima,T., Furuno,M., Futaki,S., Gariboldi,M., Georgii-Hemming,P., Gingeras,T.R., Gojobori,T., Green,R.E., Gustincich,S., Harbers,M., Hayashi,Y., Hensch,T.K., Hirokawa,N., Hill,D., Huminiecki,L., Iacono,M., Ikeo,K., Iwama,A., Ishikawa,T., Jakt,M., Kanapin,A., Katoh,M., Kawasawa,Y., Kelso,J., Kitamura,H., Kitano,H., Kollias,G., Krishnan,S.P., Kruger,A., Kummerfeld,S.K., Kurochkin,I.V., Lareau,L.F., Lazarevic,D., Lipovich,L., Liu,J., Liuni,S., McWilliam,S., Madan Babu,M., Madera,M., Marchionni,L., Matsuda,H., Matsuzawa,S., Miki,H., Mignone,F., Miyake,S., Morris,K., Mottagui-Tabar,S., Mulder,N., Nakano,N., Nakauchi,H., Ng,P., Nilsson,R., Nishiguchi,S., Nishikawa,S., Nori,F., Ohara,O., Okazaki,Y., Orlando,V., Pang,K.C., Pavan,W.J., Pavesi,G., Pesole,G., Petrovsky,N., Piazza,S., Reed,J., Reid,J.F., Ring,B.Z., Ringwald,M., Rost,B., Ruan,Y., Salzberg,S.L., Sandelin,A., Schneider,C., Schonbach,C., Sekiguchi,K., Semple,C.A., Seno,S., Sessa,L., Sheng,Y., Shibata,Y., Shimada,H., Shimada,K., Silva,D., Sinclair,B., Sperling,S., Stupka,E., Sugiura,K., Sultana,R., Takenaka,Y., Taki,K., Tammoja,K., Tan,S.L., Tang,S., Taylor,M.S., Tegner,J., Teichmann,S.A., Ueda,H.R., van Nimwegen,E., Verardo,R., Wei,C.L., Yagi,K., Yamanishi,H., Zabarovsky,E., Zhu,S., Zimmer,A., Hide,W., Bult,C., Grimmond,S.M., Teasdale,R.D., Liu,E.T., Brusic,V., Quackenbush,J., Wahlestedt,C., Mattick,J.S., Hume,D.A., Kai,C., Sasaki,D., Tomaru,Y., Fukuda,S., Kanamori-Katayama,M., Suzuki,M., Aoki,J., Arakawa,T., Iida,J., Imamura,K., Itoh,M., Kato,T., Kawaji,H., Kawagashira,N., Kawashima,T., Kojima,M., Kondo,S., Konno,H., Nakano,K., Ninomiya,N., Nishio,T., Okada,M., Plessy,C., Shibata,K., Shiraki,T., Suzuki,S., Tagami,M., Waki,K., Watahiki,A., Okamura-Oho,Y., Suzuki,H., Kawai,J. and Hayashizaki,Y.

**CONSRM** FANTOM Consortium; RIKEN Genome Exploration Research Group and Genome Science Group (Genome Network Project Core Group)

**TITLE** The transcriptional landscape of the mammalian genome

**JOURNAL** Science 309 (5740), 1559-1563 (2005)

**PUBMED** 16141072

**REMARK** NUCLEOTIDE SEQUENCE [LARGE SCALE RNA] (ISOFORMS 1 AND 2).  
STRAIN=C57BL/6J; TISSUE=Aorta, Bone marrow, Eye, Placenta, Retina, Urinary bladder, and Vein  
Erratum:[Science. 2006 Mar 24;311(5768):1713]

**REFERENCE** 3 (residues 1 to 504)

**AUTHORS** Gerhard,D.S., Wagner,L., Feingold,E.A., Shenmen,C.M., Grouse,L.H., Schuler,G., Klein,S.L., Old,S., Rasooly,R., Good,P., Guyer,M., Peck,A.M., Derge,J.G., Lipman,D., Collins,F.S., Jang,W., Sherry,S., Feolo,M., Misquitta,L., Lee,E., Rotmistrovsky,K., Greenhut,S.F., Schaefer,C.F., Buetow,K., Bonner,T.I., Haussler,D., Kent,J., Kiekhaus,M., Furey,T., Brent,M., Prange,C., Schreiber,K., Shapiro,N., Bhat,N.K., Hopkins,R.F., Hsie,F., Driscoll,T., Soares,M.B., Casavant,T.L., Scheetz,T.E., Brown-stein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Piao,Y., Dudekula,D.B., Ko,M.S., Kawakami,K., Suzuki,Y., Sugano,S., Gruber,C.E., Smith,M.R., Simmons,B., Moore,T., Waterman,R., Johnson,S.L., Ruan,Y., Wei,C.L., Mathavan,S., Gunaratne,P.H., Wu,J., Garcia,A.M., Hulyk,S.W., Fuh,E., Yuan,Y., Snead,A., Kowis,C., Hodgson,A., Muzny,D.M., McPherson,J., Gibbs,R.A., Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madari,A., Young,A.C., Wetherby,K.D., Granite,S.J., Kwong,P.N., Brinkley,C.P., Pearson,R.L., Bouffard,G.G., Blakesly,R.W.,

Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J.,  
Myers,R.M., Butterfield,Y.S., Griffith,M., Griffith,O.L.,  
Krzywinski,M.I., Liao,N., Morin,R., Palmquist,D., Petrescu,A.S.,  
Skalska,U., Smailus,D.E., Stott,J.M., Schnurch,A., Schein,J.E.,  
Jones,S.J., Holt,R.A., Baross,A., Marra,M.A., Clifton,S.,  
Makowski,K.A., Bosak,S. and Malek,J.

CONSRM MGC Project Team

TITLE The status, quality, and expansion of the NIH full-length cDNA  
project: the Mammalian Gene Collection (MGC)

JOURNAL Genome Res. 14 (10B), 2121-2127 (2004).

PUBMED 15489334

REMARK NUCLEOTIDE SEQUENCE [LARGE SCALE mRNA] (ISOFORM 1).  
TISSUE=Trophoblast stem cell  
Erratum:[Genome Res. 2006 Jun;16(6):804. Morrin, Ryan [corrected to  
Morrin, Ryan]]

COMMENT On or before Sep 7, 2006 this sequence version replaced  
gi:81883617, gi:81897952.  
[FUNCTION] Beta-1,3-N-acetylgalactosaminyltransferase active in  
synthesizing a unique carbohydrate structure,  
GalNAc-beta-1-3GlcNAc, on N- and O-glycans. Has no galactose nor  
galactosaminyl transferase activity toward any acceptor substrate  
(By similarity).  
[PATHWAY] Protein modification; protein glycosylation.  
[SUBCELLULAR LOCATION] Golgi apparatus membrane; Single-pass type  
II membrane protein (By similarity).  
[ALTERNATIVE PRODUCTS] Event=Alternative splicing; Named  
isoforms=2; Name=1; IsoId=Q8BG28-1; Sequence=Displayed; Name=2;  
IsoId=Q8BG28-2; Sequence=VSP\_020253, VSP\_020254; Note=No  
experimental confirmation available.  
[TISSUE SPECIFICITY] Present in testis (at protein level). In  
testis, it is mainly detected in the middle layers of seminiferous  
tubules at stages XII to II. Strongly expressed in primary and  
secondary spermatocytes and early round spermatids, but not in  
spermatogonia, elongating or elongated spermatids, or in Leydig or  
Sertoli cells.  
[PTM] N-glycosylated (By similarity).  
[SIMILARITY] Belongs to the glycosyltransferase 31 family.

FEATURES Location/Qualifiers

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Protein 1..504  
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/inference="non-experimental evidence, no additional details recorded"  
/note="Lumenal (Potential)."  
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/note="S -> P (in Ref. 3; AAH85110)."  
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/note="S -> G (in Ref. 3; AAH85110)."

## ORIGIN

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241 hrvtvndggg vlrvlaageg alphefmegv egvaggfiyt vqegdallrs lysrpqrлад  
301 hiqdlqveda llgeessvhd divfvvdvdt yrnpaklln fyrwtvests fdll1ktddd  
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481 eelsklwelk elcgdp cqce akvr

//

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PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

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Display GenBank Show 5 Send to Hide:  sequence  all but gene, CDS and mRNA

Range: from  to   Reverse complemented strand Features:

1: AK035259. Reports *Mus musculus* adul...[gi:26330547]

Links

Comment Features Sequence

LOCUS AK035259 2399 bp mRNA linear HTC 03-OCT-2006  
 DEFINITION *Mus musculus* adult male urinary bladder cDNA, RIKEN full-length enriched library, clone:9530006I10 product:hypothetical Glycosyltransferase family 31 containing protein, full insert sequence.  
 ACCESSION AK035259  
 VERSION AK035259.1 GI:26330547  
 KEYWORDS HTC; HTC\_FLI; CAP trapper.  
 SOURCE *Mus musculus* (house mouse)  
 ORGANISM *Mus musculus*  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
 REFERENCE 1  
 AUTHORS Carninci, P. and Hayashizaki, Y.  
 TITLE High-efficiency full-length cDNA cloning  
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
 PUBMED 10349636  
 REFERENCE 2  
 AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
 PUBMED 11042159  
 REFERENCE 3  
 AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
 TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer  
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)  
 PUBMED 11076861  
 REFERENCE 4  
 AUTHORS Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,

Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L.M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyo-oka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. and Hayashizaki, Y.

CONSRM	RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium
TITLE	Functional annotation of a full-length mouse cDNA collection
JOURNAL	Nature 409 (6821), 685-690 (2001)
PUBMED	<u>11217851</u>
REFERENCE	5
AUTHORS	Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.
CONSRM	FANTOM Consortium; RIKEN Genome Exploration Research Group Phase I & II Team
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL	Nature 420 (6915), 563-573 (2002)
PUBMED	<u>12466851</u>
REFERENCE	6
AUTHORS	Carninci, P., Kasukawa, T., Katayama, S., Gough, J., Frith, M.C., Maeda, N., Oyama, R., Ravasi, T., Lenhard, B., Wells, C., Kodzius, R., Shimokawa, K., Bajic, V.B., Brenner, S.E., Batalov, S., Forrest, A.R., Zavolan, M., Davis, M.J., Wilming, L.G., Aidinis, V., Allen, J.E., Ambesi-Impiombato, A., Apweiler, R., Aturaliya, R.N., Bailey, T.L., Bansal, M., Baxter, L., Beisel, K.W., Bersano, T., Bono, H., Chalk, A.M.,

Chiu,K.P., Choudhary,V., Christoffels,A., Clutterbuck,D.R.,  
 Crowe,M.L., Dalla,E., Dalrymple,B.P., de Bono,B., Della Gatta,G.,  
 di Bernardo,D., Down,T., Engstrom,P., Fagiolini,M., Faulkner,G.,  
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 Georgii-Hemming,P., Gingeras,T.R., Gojobori,T., Green,R.E.,  
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 Hill,D., Huminiecki,L., Iacono,M., Ikeo,K., Iwama,A., Ishikawa,T.,  
 Jakt,M., Kanapin,A., Katoh,M., Kawasawa,Y., Kelso,J., Kitamura,H.,  
 Kitano,H., Kollias,G., Krishnan,S.P., Kruger,A., Kummerfeld,S.K.,  
 Kurochkin,I.V., Lareau,L.F., Lazarevic,D., Lipovich,L., Liu,J.,  
 Liuni,S., McWilliam,S., Madan Babu,M., Madera,M., Marchionni,L.,  
 Matsuda,H., Matsuzawa,S., Miki,H., Mignone,F., Miyake,S.,  
 Morris,K., Mottagui-Tabar,S., Mulder,N., Nakano,N., Nakauchi,H.,  
 Ng,P., Nilsson,R., Nishiguchi,S., Nishikawa,S., Nori,F., Ohara,O.,  
 Okazaki,Y., Orlando,V., Pang,K.C., Pavan,W.J., Pavesi,G.,  
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 Sessa,L., Sheng,Y., Shibata,Y., Shimada,H., Shimada,K., Silva,D.,  
 Sinclair,B., Sperling,S., Stupka,E., Sugiura,K., Sultana,R.,  
 Takenaka,Y., Taki,K., Tammoja,K., Tan,S.L., Tang,S., Taylor,M.S.,  
 Tegner,J., Teichmann,S.A., Ueda,H.R., van Nimwegen,E., Verardo,R.,  
 Wei,C.L., Yagi,K., Yamanishi,H., Zabarovsky,E., Zhu,S., Zimmer,A.,  
 Hide,W., Bult,C., Grimmond,S.M., Teasdale,R.D., Liu,E.T.,  
 Brusic,V., Quackenbush,J., Wahlestedt,C., Mattick,J.S., Hume,D.A.,  
 Kai,C., Sasaki,D., Tomaru,Y., Fukuda,S., Kanamori-Katayama,M.,  
 Suzuki,M., Aoki,J., Arakawa,T., Iida,J., Imamura,K., Itoh,M.,  
 Kato,T., Kawaji,H., Kawagashira,N., Kawashima,T., Kojima,M.,  
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 Plessy,C., Shibata,K., Shiraki,T., Suzuki,S., Tagami,M., Waki,K.,  
 Watahiki,A., Okamura-Oho,Y., Suzuki,H., Kawai,J. and Hayashizaki,Y.

CONSRM

FANTOM Consortium; RIKEN Genome Exploration Research Group and  
 Genome Science Group (Genome Network Project Core Group)

TITLE

The transcriptional landscape of the mammalian genome

JOURNAL

Science 309 (5740), 1559-1563 (2005)

16141072

REMARK

Erratum: [Science. 2006 Mar 24;311(5768):1713]

REFERENCE

7

Katayama,S., Tomaru,Y., Kasukawa,T., Waki,K., Nakanishi,M.,  
 Nakamura,M., Nishida,H., Yap,C.C., Suzuki,M., Kawai,J., Suzuki,H.,  
 Carninci,P., Hayashizaki,Y., Wells,C., Frith,M., Ravasi,T.,  
 Pang,K.C., Hallinan,J., Mattick,J., Hume,D.A., Lipovich,L.,  
 Batalov,S., Engstrom,P.G., Mizuno,Y., Faghiri,M.A., Sandelin,A.,  
 Chalk,A.M., Mottagui-Tabar,S., Liang,Z., Lenhard,B. and  
 Wahlestedt,C.

CONSRM

RIKEN Genome Exploration Research Group; Genome Science Group  
 (Genome Network Project Core Group); FANTOM Consortium

TITLE

Antisense transcription in the mammalian transcriptome

JOURNAL

Science 309 (5740), 1564-1566 (2005)

16141073

REFERENCE

8 (bases 1 to 2399)

AUTHORS

Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,  
 Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,  
 Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,  
 Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,  
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 Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,  
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 Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,

Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,  
 Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,  
 Muramatsu, M. and Hayashizaki, Y.

**TITLE** Direct Submission

**JOURNAL** Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL:<http://genome.gsc.riken.jp/>, Tel:81-45-503-9222, Fax:81-45-503-9216)

**COMMENT** cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
 Please visit our web site for further details.  
[URL:<http://genome.gsc.riken.jp/>](http://genome.gsc.riken.jp/)  
[URL:<http://fantom.gsc.riken.jp/>](http://fantom.gsc.riken.jp/).

**FEATURES** Location/Qualifiers

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 /db\_xref="taxon:10090"  
 /clone="9530006I10"  
 /sex="male"  
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 /clone\_lib="RIKEN full-length enriched mouse cDNA library"  
 /dev\_stage="adult"

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 (The translation sequence is a long string of amino acid codes from M to R, including several gaps and stop codons.)

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**polyA\_site** 2399  
 /note="putative"

**ORIGIN**

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